

In the Claims

Please amend Claims 22, 32, and 42. Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (pages i-iii).

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22. (Amended) A method of determining nucleotide identity of at least one nucleotide position of a polynucleotide of interest, comprising the steps of;
- a) contacting the polynucleotide of interest with a population of single-stranded primers, wherein said population of single-stranded primers comprises at least two oligonucleotides of different lengths, wherein said oligonucleotides have known sequences, such that at least one oligonucleotide hybridizes to the polynucleotide of interest immediately adjacent to each nucleotide position of interest to be identified, generating template-single-stranded primer complexes;
 - b) subjecting said complexes to a single base extension reaction to extend each hybridized primer by a terminating nucleotide, generating extended primers;
 - c) separating said extended primers from each other; and
 - d) identifying each terminating nucleotide that has been added to each extended primer, thereby determining the identity of at least one nucleotide position of a polynucleotide of interest.
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32. (Amended) A method of analyzing a nucleotide sequence of a polynucleotide of interest for the presence or absence of one or more alterations, wherein the sequence of the polynucleotide of interest is generally known, and wherein nucleotide identity of at least one nucleotide position of a polynucleotide of interest is determined, comprising the steps of;
- a) contacting said polynucleotide of interest with a population of single-stranded primers, wherein said population of single-stranded primers comprises at least two oligonucleotides of different lengths and wherein said oligonucleotides have known sequences, such that at least one oligonucleotide hybridizes immediately adjacent to each potential alteration in the polynucleotide of interest, generating template-single-stranded primer complexes;

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- b) subjecting said complexes to a single base extension reaction to extend each hybridized primer by the addition of a terminating nucleotide, generating extended primers;
 - c) separating said extended primers from each other;
 - d) identifying each terminating nucleotide that has been added to each extended primer; and
 - e) comparing said identified nucleotide with the sequence of the polynucleotide of interest, whereby the presence or absence of one or more alterations is determined.
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42. (Amended) A method for determining nucleotide identity of at least one nucleotide position of a polynucleotide of interest, comprising the steps of;

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- a) contacting said polynucleotide of interest with a population of single-stranded primers, wherein said single-stranded primers comprise an array of one or more sets of one or more oligonucleotides, wherein at least one set comprises at least two oligonucleotides that are substantially homologous but differ from each other by one base at their 3' termini, wherein the oligonucleotides of the array have known sequence and wherein each oligonucleotide is attached to a solid support at a known location, to form the array, wherein at least one oligonucleotide of the array hybridizes to said polynucleotide of interest immediately adjacent to each nucleotide position to be identified, generating template-single-stranded primer complexes;
 - b) subjecting said complexes to a single base extension reaction to extend each annealed primer by a terminating nucleotide, generating extended primers; and
 - c) identifying each terminating nucleotide that has been added to each primer; thereby determining the identity of at least one nucleotide position of a polynucleotide of interest.
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